

OIEP

RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/870,122

TIME: 10:25:07

Input Set : A:\PCT-US99-28826 Sequence listing.txt
 Output Set: N:\CRF3\11212001\I870122.raw

ENTERED

4 <110> APPLICANT: Regents of the University of Minnesota et al.
 6 <120> TITLE OF INVENTION: Streptococcal C5a peptidase vaccine
 8 <130> FILE REFERENCE: 600.450W01
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/870,122
 C--> 10 <141> CURRENT FILING DATE: 2001-05-30
 10 <150> PRIOR APPLICATION NUMBER: US 09/206,898
 11 <151> PRIOR FILING DATE: 1998-12-07
 13 <150> PRIOR APPLICATION NUMBER: US 08/589,756
 14 <151> PRIOR FILING DATE: 1996-01-22
 16 <160> NUMBER OF SEQ ID NOS: 23
 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1164
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Streptococcus pyogenes
 25 <400> SEQUENCE: 1

26	Leu	Arg	Lys	Lys	Gln	Lys	Leu	Pro	Phe	Asp	Lys	Leu	Ala	Ile	Ala	Leu
27	1				5					10					15	
28	Met	Ser	Thr	Ser	Ile	Leu	Leu	Asn	Ala	Gln	Ser	Asp	Ile	Lys	Ala	Asn
29				20					25					30		
30	Thr	Val	Thr	Glu	Asp	Thr	Pro	Ala	Thr	Glu	Gln	Ala	Val	Glu	Thr	Pro
31			35					40					45			
32	Gln	Pro	Thr	Thr	Val	Ser	Glu	Glu	Val	Pro	Ser	Ser	Lys	Glu	Thr	Lys
33		50					55				60					
34	Thr	Pro	Gln	Thr	Pro	Asp	Asp	Ala	Glu	Glu	Thr	Val	Ala	Asp	Asp	Ala
35	65				70					75					80	
36	Asn	Asp	Leu	Ala	Pro	Gln	Ala	Pro	Ala	Lys	Thr	Pro	Asp	Thr	Ser	Ala
37				85					90					95		
38	Thr	Ser	Lys	Ala	Thr	Ile	Arg	Asp	Leu	Asn	Asp	Pro	Ser	Gln	Val	Lys
39				100					105					110		
40	Thr	Leu	Gln	Glu	Lys	Ala	Gly	Lys	Gly	Ala	Gly	Thr	Val	Val	Ala	Val
41			115					120					125			
42	Ile	Asp	Ala	Gly	Phe	Asp	Lys	Asn	His	Glu	Ala	Trp	Arg	Leu	Thr	Asp
43		130					135					140				
44	Lys	Ala	Lys	Ala	Arg	Tyr	Gln	Ser	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Lys
45		145				150				155				160		
46	Lys	Glu	His	Gly	Ile	Thr	Tyr	Gly	Glu	Trp	Val	Asn	Asp	Lys	Val	Ala
47				165					170					175		
48	Tyr	Tyr	His	Asp	Tyr	Ser	Lys	Asp	Gly	Lys	Thr	Ala	Val	Asp	Gln	Glu
49			180					185						190		
50	His	Gly	Thr	His	Val	Ser	Gly	Ile	Leu	Ser	Gly	Asn	Ala	Pro	Ser	Glu
51			195					200					205			
52	Thr	Lys	Glu	Pro	Tyr	Arg	Leu	Glu	Gly	Ala	Met	Pro	Glu	Ala	Gln	Leu
53		210					215					220				
54	Leu	Leu	Met	Arg	Val	Glu	Ile	Val	Asn	Gly	Leu	Ala	Asp	Tyr	Ala	Arg
55		225				230				235				240		
56	Asn	Tyr	Ala	Gln	Ala	Ile	Arg	Asp	Ala	Val	Asn	Leu	Gly	Ala	Lys	Val

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57          245          250          255
58   Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
59          260          265          270
60   Asp Glu Thr Lys Lys Pro Phe Val Tyr Ala Lys Ser Lys Gly Val Arg
61          275          280          285
62   Ile Val Thr Thr Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
63          290          295          300
64   Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
65          305          310          315          320
66   Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Asn Gln
67          325          330          335
68   Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
69          340          345          350
70   Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
71          355          360          365
72   Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
73          370          375          380
74   Lys Gly Lys Ile Ala Leu Ile Glu Arg Ser Asp Ile Asp Phe Thr Asp
75          385          390          395          400
76   Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
77          405          410          415
78   Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
79          420          425          430
80   Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
81          435          440          445
82   Asn Ser Gln Lys Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
83          450          455          460
84   Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
85          465          470          475          480
86   Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
87          485          490          495
88   Leu Ser Ser Ala Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
89          500          505          510
90   Met Ser Ala Pro Leu Val Ala Val Ile Met Gly Leu Leu Gln Lys Gln
91          515          520          525
92   Tyr Glu Thr Gln Tyr Pro Asp Met Thr Gln Ser Glu Arg Leu Asp Leu
93          530          535          540
94   Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
95          545          550          555          560
96   Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
97          565          570          575
98   Ala Lys Lys Ala Ser Glu Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
99          580          585          590
100  Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
101          595          600          605
102  Thr Val Thr Val His Asn Lys Ser Asp Lys Pro His Glu Leu Tyr Tyr
103          610          615          620
104  Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
105          625          630          635          640

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106  Ala Pro Lys Ala Leu Ile Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
107              645              650              655
108  Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Ile Ser Gln Phe
109              660              665              670
110  Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
111              675              680              685
112  Phe Val Arg Ile Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
113              690              695              700
114  Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
115              705              710              715              720
116  Lys Pro Leu Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Glu
117              725              730              735
118  Ile Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
119              740              745              750
120  Ala Leu Lys Asn Asp Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
121              755              760              765
122  Thr Ile Ile Asn Val Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
123              770              775              780
124  Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
125              785              790              795              800
126  Gln Asp Asp Asp Arg His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
127              805              810              815
128  Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
129              820              825              830
130  Gln Phe His Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
131              835              840              845
132  Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
133              850              855              860
134  Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
135              865              870              875              880
136  Thr Arg Phe Glu Ile Ser Arg Trp Asp Gly Lys Asp Lys Asp Ala Lys
137              885              890              895
138  Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
139              900              905              910
140  Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
141              915              920              925
142  Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
143              930              935              940
144  Arg Arg Leu Thr Leu Ala Ser Lys Pro Gln Thr Ser Gln Pro Val Tyr
145              945              950              955              960
146  Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
147              965              970              975
148  Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
149              980              985              990
150  Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
151              995              1000              1005
152  Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
153              1010              1015              1020
154  Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser

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155      1025              1030              1035              1040
156  Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
157              1045              1050              1055
158  Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Gly Gln Asp
159              1060              1065              1070
160  Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
161              1075              1080              1085
162  Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro
163              1090              1095              1100
164  Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
165              1105              1110              1115              1120
166  Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn
167              1125              1130              1135
168  Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly Leu
169              1140              1145              1150
170  Val Ala His Ile Phe Lys Thr Lys Arg Thr Glu Asp
171              1155              1160
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 1167
175 <212> TYPE: PRT
176 <213> ORGANISM: Streptococcus pyogenes
178 <400> SEQUENCE: 2
179  Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
180    1          5          10          15
181  Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
182          20          25          30
183  Thr Val Thr Glu Asp Thr Pro Val Thr Glu Gln Ala Val Glu Thr Pro
184          35          40          45
185  Gln Pro Thr Ala Val Ser Glu Val Pro Ser Ser Lys Glu Thr Lys
186          50          55          60
187  Thr Pro Gln Thr Pro Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
188          65          70          75          80
189  Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
190          85          90          95
191  Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
192          100         105         110
193  Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
194          115         120         125
195  Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
196          130         135         140
197  Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
198          145         150         155         160
199  Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
200          165         170         175
201  Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
202          180         185         190
203  His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
204          195         200         205
205  Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu

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206	210	215	220
207	Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg		
208	225	230	235
209	Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val		
210		245	250
211	Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro		
212		260	265
213	Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser		
214		275	280
215	Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg		
216		290	295
217	Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala		
218	305	310	315
219	Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln		
220		325	330
221	Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu		
222		340	345
223	Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp		
224		355	360
225	Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val		
226		370	375
227	Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp		
228	385	390	395
229	Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr		
230		405	410
231	Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln		
232		420	425
233	Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp		
234		435	440
235	Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro		
236		450	455
237	Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr		
238	465	470	475
239	Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile		
240		485	490
241	Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser		
242		500	505
243	Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln		
244		515	520
245	Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu		
246		530	535
247	Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp		
248	545	550	555
249	Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp		
250		565	570
251	Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn		
252		580	585
253	Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val		
254		595	600

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/870,122

DATE: 12/05/2001

TIME: 10:25:08

Input Set : A:\PCT-US99-28826 Sequence listing.txt.txt

Output Set: N:\CRF3\11212001\I870122.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date